

STIC Biotechnology Systems Branch

1 FWO

CRF Problem Report

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: 10/554,238
Filing Date: 10/20/05
Date Processed by STIC: 2/23/07

STIC Contact: Mark Spencer: Telephone: 571-272-2510; Fax: 571-273-0221

Nature of CRF Problem:

- ☐ (circle one) Damaged or Unreadable (for Unreadable, see attached)
- ☐ Blank (no files on CRF) (see attached)
- ☐ Empty file (filename present, but no bytes in file) (see attached)
- ☐ Wrong file saved to CRF (invention title, docket number, or applicant(s) do not match those in official application) (see attached)
- ☐ Not saved in ASCII text
- ☐ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.
- ☐ Did not contain a Sequence Listing. (see attached sample)
- ☒ Other:
sequence listing was split into separate files

**PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM TO REDUCE ERRORS.
SEE BELOW FOR ADDRESS:**

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/20/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/554,238

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 1 Wrapped Aminos
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 3 Numbering
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 6 "bug"
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
Response scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 12 "bug"
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

10/554,238

SEQUENCE LISTING ← do NOT use bold font

2

```
<110> Breitenstein, Antje
<120> Method for the Detection of Bacteria of the Genus Legionella
<140> US 10/554,238
<141> 2005-10-20
<160> 8
<210> 1
<211> 19
<212> DNA
<213> Legionella pneumophila
<400> 1
<400> ttcgcccgcg tctgtatcg
<210> 2
<211> 18
<212> DNA
<213> Legionella pneumophila
<400> 2
<400> atctgaccgt cccaggtt
<210> 3
<211> 20
<212> DNA
<213> Legionella feelei
<400> 3
<400> gcgccactaa cctcattcat
<210> 4
<211> 20
<212> DNA
<213> Legionella feelei
<400> 4
<400> tatacaacca cctacgcacc
```

Per 1.823
of sequence
rules

use a
fixed-width
font

19 ← insert cumulative
base total at
right margin of each line

18 ←

20 ←

20 ←

The above was one of the non-ASCII files on
submitted disk
"Sequence Listing1.DOC"
(see item 4 on Error
summary sheet)

See next page

please
re-arrange
<400> →
line
as shown.
It does
NOT
appear on
same line
as bases
or amino
acids

<210> 5
 <211> 20
 <212> DNA
 <213> Legionella jordanis
 <400> 5
~~<400>~~ cttacgggtcc ccagcttttt

206

<210> 6
 <211> 20
 <212> DNA
 <213> Legionella jordanis
 <400> 6
~~<400>~~ ccactcctcc ccaactgaaag

206

<210> 7
 <211> 19
 <212> DNA
 <213> Legionella sp.
 <400> 7
~~<400>~~ cctcctcccc actgaaagt

196

<210> 8
 <211> 20
 <212> DNA
 <213> Legionella sp.
 <400> 8
~~<400>~~ cactgtatgt caagggtagg

206

The above was the other file on submitted
 disk "Sequence Listing 2. Doc"

DO NOT split a sequence listing file.

Per 1.824 of Sequence Rules, the sequence
 listing must be one file on submitted
 computer readable
 form

Please consult Sequence Rules
 for valid format